



High quality sequence start: 14  
High quality sequence stop: 663.

FEATURES  
Location/Qualifiers  
1..670

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BN0034"  
/dev\_stage="Adult"

/note="Organ: Breast, normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 227 a 109 c 164 g 170 t  
ORIGIN

Query Match 39.6%; Score 612; DB 11; Length 670;  
Best Local Similarity 97.3%; Pred. No. 1.9e-139;  
Matches 644; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

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OY 188 caattatgaagaacagaccacccaacacattatatacagatgtccagtgg 247
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Db 4 ctctacatgaaaaacagacac--aaagccaaacatttatcagatgtccagtgg 61
OY 248 actactgttatagagaacattcattgatatctccagaggaaaggagaaatgaca 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 actactgttatagagaacattcattgatatctccagaggaaaggagaaatgaca 121
OY 308 gaagatcaccagctgttagcagacagactgcagagcaagaagaagaagaatgtgt 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 gaagatcaccagctgttagcagacagactgcagagcaagaagaagaagaatgtgt 181
OY 368 agtccactcacaacattgataatagagaagaagaagaatgtgtccctacacccat 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 agtccactcacaacattgataatagagaagaagaagaatgtgtccctacacccat 241
OY 428 cataaagaagaagaagaatgtgtgtgacatttgaaactactagtaagagcacttt 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 catataaagaagaagaagaatgtgtgtgacatttgaaactactagtaagagcacttt 301
OY 488 gggagaagtatttggttcgagagaagaagaatgtgt-aaatactatgctatgaattct 546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 gggagaagtatttggttcgagagaagaagaatgtgt-aaatactatgctatgaattct 361
OY 547 gaagaagaagaatcattatgtcaaaagatgaagtgcacacactcaactgaagcagagt 606
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 gaagaagaagaatcattatgtcaaaagatgaagtgcacacactcaactgaagcagagt 421
OY 607 attaaagaacactagacatcccttttaacatcccttgaaatatccctccagacaaaga 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 attaaagaacactagacatcccttttttaacatcccttgaaatatccctccagacaaaga 481
OY 667 ccgtttgtgttgatgagaaatgtatgtggggcgagcgtgttttccatttgcgag 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 ccgtttgtgttgatgagaaatgtatgtggggcgagcgtgttttccatttgcgag 541
OY 727 agagcgggtgtctctgagagccgacacglttctatagtgagagaatgtcttgcctt 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 agagcgggtgtctctgagagccgacacglttctatagtgagagaatgtcttgcctt 601
OY 787 ggactatctacatcccgaaagaatgtgtacccgtgactcgaagtgtgagaatcctaagt 846
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 ggactatctacatcccgaaagaatgtgtacccgtgactcgaagtgtgagaatcctaagt 661
OY 847 gg 848
    |||
Db 662 gg 663
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RESULT 2

BE779151 876 bp mRNA EST 20-OCT-2000  
601464773F1 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:3867931 5',  
LOCUS  
DEFINITION  
mRNA sequence.  
ACCESSION  
BE779151  
VERSION  
BE779151.1 GI:10200349  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 876)  
NIH-MGC <http://imgc.nci.nih.gov/>.  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC).  
UNPUBLISHED (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgapsd-remail.nih.gov](mailto:cgapsd-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LMA9615 row: a column: 20  
High quality sequence start: 6  
High quality sequence stop: 660.

FEATURES  
Location/Qualifiers  
1..876

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:3867931"  
/clone\_lib="NIH\_MGC\_67"  
/tissue\_type="retinoblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."

BASE COUNT 301 a 163 c 217 g 195 t  
ORIGIN

Query Match 33.8%; Score 523.4; DB 10; Length 876;  
Best Local Similarity 89.4%; Pred. No. 1e-117;  
Matches 691; Conservative 0; Mismatches 61; Indels 21; Gaps 11;

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OY 1 gggagtcacatcagagatgttaccattgtgaagaaggttggttcagaagaaggagaga 60
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Db 17 ggagtcacatcagagatgttaccattgtgaagaaggttggttcagaagaaggagaga 76
OY 61 atataaanaaacctggagcccaagatctccctttgagagagatggtcttcaatag 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 atataaanaaacctggagcccaagatctccctttgagagagatggtcttcaatag 136
OY 121 atataaagaacacctcaagatgtgattacccttaccctcacaacttccagtgc 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 atataaagaacacctcaagatgtgattacccttaccctcacaacttccagtgc 196
OY 181 aaatggccgtttaagaacacgaagacccaagaacacacacatataatcaatgtct 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 aaatggccgtttaagaacacgaagacccaagaacacacacatataatcaatgtct 256
OY 241 ccagtgactactgttatagagaagaacatttcaatgatatccagaggaagaaggaga 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 ccagtgactactgttatagagaagaacatttcaatgatatccagaggaagaaggaga 316
OY 301 atgacagaagctatccaggtctgttagcagacagactgcagaagcagaagaagagagaat 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 atgacagaagctatccaggtctgttagcagacagactgcagaagcagaagaagagagaat 376
OY 361 gaattgtagtcacaacttcaacaatgtataatagagagagaagaatgagatgcctctac 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 377 GAATGTAGTCCAACTTCACAAATTGATATATAGAGAGGAAGAGATGATGCTCTTAC 436

Qy 421 aaccatcataaagaagaacaatgaatatttgactatttgaaactactggttaag 480

Db 437 AA-CCATCATTAAGAAAGAAACATGATGATTTTGACTATTTGAAACTACTAGTAAAG 495

Qy 481 cacttttggaaagtatttgcttcgagaagaagcaagtggaaaa-tactatgctata 539

Db 496 CACTTT--GGGAAGTATTATTGTTGCGAGAGAGCAAGTGGAAAACTCTATGCTATGA 553

Qy 540 aga-ttcgagaagaaga-gtcattattgcaagaagatgaagtgcacacac---tctaac 594

Db 554 AGATTCTGGAAGAAAGAAAGAGTTCATTCAGCAAGATGACCTGGCACCACTCCTTAC 613

Qy 555 tgaagc---agagtatttaagaacactag---acatcccttttaactcctt---gaa 645

Db 614 TGAAGGCCAGAGATTAATTAACAGACACTGACATTCCTTTTAAACCTCTTGAAAA 673

Qy 646 atattccttcaga--caaaagacgcttgcttgcttgcttgcttgcttgcttgcttgct 702

Db 674 TTATTCCTTCCAGACCAGAGACCCGCTGAGCTAGCTGATGACTATGTTAATGTGGGC 733

Qy 703 cgaagctgtttccatttgcagagagcggtgtctctcctcgcagaccgcacac 755

Db 734 GAAGCTGATGTGTCATATGTGAGAGACGGGGTTCGAGAGCAAGACAGCTAC 786

RESULT 3

LOCUS AM960221 607 bp mRNA EST 01-JUN-2000

DEFINITION EST372292 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.

ACCESSION AM960221

VERSION AM960221.1 GI:8149905

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 607)

AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,J., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)

COMMENT Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johnq@tigr.org  
Plate: 143

FEATURES

source 1..607

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="MAGE resequences, MAGF"

/note="Vector: pBluescriptSkm"

BASE COUNT 221 a 104 c 147 g 135 t

ORIGIN

Query Match 32.8%, Score 507.4; DB 10; Length 607;

Best Local Similarity 97.9%; Pred. No. 8e-114;

Matches 514; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 gggagtcacatgagcagctgttaccatgtgaaagaaggttggttcgaaaggaggaga 60

Db 83 GGGAGTCATCATGAGCGATGTTACCATGTTGAAAGAGGTTGGTTCAAGAGGGGAGA 142

Qy 61 atataaaaaactggaagccaagatacttcttctgaagaagaatggtcattcatag 120

Db 143 ATATATAAAAACTGGAGCCCAAGATACCTCTTTTGAAGACAGATGCTCATTTAGG 202

Qy 121 atataaagaagaaccctcaagatgtagatttacttctccctcaaaacttttcagtc 180

Db 203 ATATTAAGAAACCTCAAGATGTGATTTACTTATCCCTCAACACTTTTCAGTGGC 262

Qy 181 aaatgccagttaatatgaagaacagacgaacgaacgaacacattatatacagatct 240

Db 263 AAATGCCAGTTATATATAAAACAGAACAGACCAAGCCAAACACATTATATAGATGCT 322

Qy 241 ccagtgactactgtatagagaacattcaatgtagatctccagagaaaggaga 300

Db 323 CCAGTGCATAGCTGATTATAGAGAGCAATTTCTATGATTTCCAGAGAAAGGAGA 382

Qy 301 atggaagaagctatccagctgtagcagacagacgctgcagagcgagaagaagaat 360

Db 383 ATGACAGAGATTCATTCAGGCTGTACACACACACGACAGCAAGAGAGAGAAAT 442

Qy 361 gaattgtagtccaaactcaaatatgataatagagaagaagaatgtagtctctac 420

Db 443 GAATTTATTCACACTTCACAAATTTGATATATAGAGAGAGAGATGATGCTTAC 502

Qy 421 aaccatcataaagaagaacaatgaatatttgactatttgaaactactagtaag 480

Db 503 AACCCATCATTAAGAAAGAAACATGATGATTTTGACTATTTGAAACTCTAGGAAAG 562

Qy 481 cacttttggaaagtatttgcttcgagaagaagcagtgaaa 525

Db 563 CACTTTTGGGAAGTATTTTGGTTGAGAGAAAGCAAGTGGAAA 607

RESULT 4

LOCUS AL548951 1000 bp mRNA EST 16-FEB-2001

DEFINITION AL548951.L1.NFL006.PL2 Homo sapiens cDNA clone CSOD1042YE16 5

ACCESSION AL548951

VERSION AL548951.1 GI:12884464

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1000)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 EVRI cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source 1..1000

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="CSOD1042YE16"

/clone\_lib="L1.NFL006.PL2"

/tissue\_type="Placenta"

/note="Vector: pCMVSPORT 6; Site:1; NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com url : http://fulllength.invitrogen.com"

BASE COUNT 219 a 289 c 289 g 189 t 14 others

ORIGIN

Query Match 32.6%, Score 503.8; DB 10; Length 1000;

Best Local Similarity 71.0%; Pred. No. 6,7e-113;  
Matches 709; Conservative 11; Mismatches 268; Indels 11; Gaps 4;

439 gacaaatgattgattgacttgaactactagtaagaagcatttgggaagtat 438  
 9 GACCAATGAACGAGTATTAGTACTGAGCTGGGCAAGGACTTTTGGCAAGGAT 68  
 499 ttgtgtcgaagaagaagctgtaaaatactatgctataaagattctgaagaaga 558  
 69 CCGKTKAAGAGAAAGGCCACAGCGC-TACTACGCCATTAAGATCTCAAGAGAGT 127  
 559 caattatgcaagaagatgaatgagacacacttaactgaagaagatataagaac 618  
 128 CACTGTGGCCAGAGAGAGTGGCCACACACTACCGAAGAACGGCTCTCGAGAATC 187  
 619 taagaccccttttaacatccttgaataatctctccagacaagaacgcttggtt 678  
 188 CAAKACCCCTTCTCTCAACGCTGAAATCTTTTCAACACGACGACGCTCTACT 247  
 679 tgtgatgaaatgtaataatgaggagagctgtttccatcttgcagagaagcggtgt 738  
 248 TTKCATGAGATAGCCCAACGGGGGAGAGCTTCTTACCTGTCCGGAGAGCTGT 307  
 739 ctctgaggagcagacagcttctatggtcagagaatgtctctgaccttgactaca 798  
 308 CTCGAGAGACGGGGCGGCTTCTATGGCTGAGATTGTGTAGCCCTGGACTAC 367  
 799 ttccggaaga---ttgtatcagtgatcacaagttgaataatcgaataatgctga 855  
 368 CTGGAGAAACAGCTGTGTACCGGGGCTCAAGCTGGAACCTCATGCTGGAAGA 427  
 856 tggccacataaaataatcagatttgaacttgcagaagaagagatcagatgcagac 915  
 428 CGGGACATTAAGATCAGACACTTCGGGGCTGTGCAAGAGGGATCAAGACGGTGCAC 487  
 916 catgaagacatctgtggaatccagaatactggcaacagaggtgttagaataatga 975  
 488 CATTAGACCTTTTGGGGCACACCTGATACCTGGCCCCGAGAGTGTGAGAGACATGA 547  
 976 ctatgacgagcagtagagcgtgtgagggcctgaagggtgtcaatgataaataatgtgtg 1035  
 548 CTACGGCCGTGACAGTGAAGTGGGGGCTGGCGGTGTATGACAGATGATGTGGG 607  
 1036 gaagttaccttctacaacacagagacatgagaacttltgaataataataatgaaga 1095  
 608 TGCGCTGCTTCTTACACAGAGACCATGGAAGCTTTTGAGCTCATCTCATGAGGA 667  
 1096 caltaattcctcgaacac-tctctcagaigcaaatcatgtcttcaaggctcttga 1154  
 668 GATCCCTTCCCGCACGCTTGGTCCGAGGCCAAGTCTTTCAGGGCTGCTCA 727  
 1155 taaagatccaataaagccttggtygagagaccagatgataaagaataatataagac 1214  
 728 AGAAGAGACCCCAAGAGAGCTTGGCGGGGCTCCAGAGCGCCAAAGGAGATATCAGC 787  
 1215 acagttctctctctgagtaaacctggaagatgataatgaataaagctgttaccctt 1274  
 788 ATGCTTCTTGGCGGTATGCTGTGGCAGACCTGTACGAARAACTAGGCCACCT 847  
 1275 ttaaacctcaagtaacatctgagacagatactagataatttgaatgaanaattacagctc 1334  
 848 TCAAGCCCCAGGTACAGTGGAGATGACACAGTATTTGATGAGAGATTCACGGCC 907  
 1335 agacttctacaataac 1394  
 908 AGATGATCAACCATCACACACATGACCA-----GATGACACATGAGATGTGTGACCA 961  
 1395 atgagagcgagcgaatttccctcaatttccactcctg 1433  
 962 GCGAGGCGRGGCCCACTTCCCACTTCTCTACTCGG 1000

RESULT 5

AL545564  
 LOCUS AL545564 1027 bp mRNA EST 16-FEB-2001  
 DEFINITION AL545564.L1.NFL006.PL2 Homo sapiens cDNA clone CS0D1015Y11.5  
 ACCESSION AL545564  
 VERSION AL545564.1 GI:12878046  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 1027)  
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 Location/Qualifiers  
 FEATURES  
 source  
 1. 1027  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1015Y11"  
 /clone\_lib="L1.NFL006.PL2"  
 /issue\_type="placenta"  
 /note="Vector: PCWVS-PORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@life.com URL :  
 http://fulllength.invitrogen.com  
 BASE COUNT 223 a 293 c 320 g 188 t 3 others  
 ORIGIN  
 Query Match 32.4%; Score 502; DB 10; Length 1027;  
 Best Local Similarity 70.7%; Pred. No. 1.8e-112;  
 Matches 724; Conservative 1; Mismatches 291; Indels 8; Gaps 4;  
 227 atataagatgtctcagtgactactgttataagagaacattatgatatctca 286  
 2 ATATCCGCTGCTCGAGTGGACCTGTCATGAGACGACCTTCCATGTGGAGACTCT 61  
 287 gaagaaaggaagaatgagacagaagctatccagctgttagcagacagactgcagagcaa 346  
 62 GAGGACGGGAGAGAGTGAGACAAACCCCATCAGCTGTGGCTGACGGCTCAAGAGCAG 121  
 347 gaagagagagaatgaatgttagtccaaacttcaaatgtataataatagaagaagag 406  
 122 GAGGAGGAGAGAGATGACTTCCGTCGGGCTCCACGAGTCAACTCAGGGCTGAAGAG 181  
 407 atgagtgccctcaaacccatc---ataaagaagaagaatgaatgaatgttacttg 463  
 182 ATGAGAGTGTCCCTGGCCAAAGCCCAAGACCGGCTGACCAATGACAGATTGAGTACT 241  
 464 aaactactagtaaaagcacttctggaagaatcttctgttgcagaagaagaagatgga 523  
 242 AAGCTCTGCGGCAAGGGCACTTTCGGCAAGGTATCTGTGTGAAGAGAAAGCCACAGC 301  
 524 aaactactatgataatgagatctgaaagaagaatcaatatttgcagaagaatgagag 583  
 302 CCTACTACGCCATGAAATCTCAAGAGAGAGTATCTGTGCAAGGACGAGTGGCC 361  
 584 caaacactactgaagaagcagatgaataaagaacacagacatccctttaaactcttg 643  
 362 CACACACTACCGAGAACCGCTCTGACAGAACTCAGGACCCCTTCTCTCAGAGCCCTG 421  
 644 aaatattccttccagacaagaacgcttgtgttctgtatgtaataatgttaatgaggc 703

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DB 422 AAGTACTCTTTCCAGACCCAGACCGCCTCTGCTTTGTATGAGTAGACCAACGGGGC 481
OY 704 gagctgttttccatttcgagagagcggtgtctctctgagaccgcacgttctat 763
DB 482 GAGCTGTTCTTCCACCTGCGCGGAACTGTGTTCTCCGAGACCGGGCCGCTTCTAT 541
OY 764 ggtgcagaatgtctctgcttgagctatctacattccggaaaga---tggtacgt 820
DB 542 GGGCTGAGATTGTGTACACCTCGTGCACCTGCACTCGAAGAAACGTGTGTCGG 601
OY 821 gatccaaagtgcagaatctatgtctgcgaagaagtgcacataaataacagattt 880
DB 602 GACCTCAAGCTGGAGAACTCATGCTGGACAAGAGCGGCACATTATGACACACTTC 661
OY 881 ggaacttgcgaagaaggatcacagatgcagccacacatgaagacattctgtgcacca 940
DB 662 GGGCTGTGCAGAGAGGGGATCAAGGACGGTCCCATGATGAGACCTTTTGGCGACACCT 721
OY 941 gaattctgcgacccagaggtgttagaagaataatgactatgcccagagtagatgtg 1000
DB 722 GAGTACTGTGCCCCCGAGGTGCTGGAGCAATGACTAGCTAGCGCTGCACTGTG 781
OY 1001 ggcctcagaggtgtcatgtatgaatgtgtggaaggttaaccttcaaccaaggac 1060
DB 782 GGGCTGGCGGTGCTCATGTACGAGATGATGTGCGGTCGCTTCTTACACAGAGAC 841
OY 1061 catggaacacttttgaatlaataatgagagaacataaattctctcgaacactctc 1120
DB 842 CATGGAAGCTTTTGTGAGCTCATCTCATGAGAGAGATCCGCTTCCCGGACGCTGT 901
OY 1121 tgaagtgaatcatgtcttcagggtc-ctgataaagatccaataaacgcttg 1178
DB 902 CCCGAGGCGCAAGTCTTCTTTCAGGGCTGCTCAARAGAAAGCAACCCAGAGAGCTTG 961
OY 1179 gtggaagacagatgatgcgaagaagaattatgagacaggttctctctggaagtaact 1238
DB 962 GGGGGGGCTCCGAGAGCGCAAGGAGATCATGAGATGCTTCTTGGCGGATGTGT 1021
OY 1239 gaca 1242
DB 1022 GGSAA 1025

RESULT 6
AL534146 864 bp mRNA EST 13-FEB-2001
LOCUS AL534146 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF005Y117 5
DEFINITION prime, mRNA sequence.
ACCESSION AL534146
VERSION AL534146.1 GI:12797639
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 864)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
Source
1..864
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF005Y117"
/clone_1ib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
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```
/note="Organ: Fetal brain; Vector: PCWMSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
PCWMSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@life.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 194 a 242 c 270 g 156 t 2 others
ORIGIN
Query Match 29.6%; Score 458.4; DB 10; Length 864;
Best Local Similarity 72.2%; Pred. No. 8.6e-102;
Matches 623; Conservative 1; Mismatches 233; Indels 6; Gaps 2.
OY 239 ctccagtgactactgtttagagagaacatttcatgtatgatactccagagaagagaa 298
DB 2 ctgcagtgagacactgtctcatcgaacgcaccttccatgtgagactctgaagacggcgag 61
OY 299 gaatgacagaagctatccaggctgtagacagaacagctgcagagcgaagaagagagaga 358
DB 62 GAGTGACAAACCGCCATCCAGACTGTGCTGACGGCTCAAGAGAGAGAGAGAGAGAG 121
OY 359 atgaattgagtcacaacttcacaatgtataataatgagagagagagatgagtcctc 418
DB 122 ATGGAATTCCTCGGCTGCGGCTCACCACCACTCAAGTGAAGAGAGATGAGGTGCTC 181
OY 419 acaaccatc---ataaagaagaagaatgaatgatttgactatttgaaactactagt 475
DB 182 CTGGCCAAACCCCAAGCAGCCGCTGACCATGAACGATTTGAGTCAAGCTGCTGGGC 241
OY 476 aaagcacttttggagaagttaatttggctcagagaagcagtggaataactatgct 535
DB 242 AAGGGCACTTTGGGCAAGGTGATCCGTGGGAAGAGAAAGCCACAGCGGCTACTAGCGC 301
OY 536 atgaagattctgagaagaagaatgaatcatttgcagaagatgagtgacacactact 595
DB 302 ATGGAATCTCTCAAGAGAGAGATCATGTGGCCAAAGAGAGAGAGTGGCCACACACTCAC 361
OY 596 gaaagcagagatlaaagaacactagacatcccttllaactcctcgaataatcttc 655
DB 362 GAGAACCGGCTCTGCAGAACTCCAGGACCCCTTCTTCAACAGCCCTGAAGTACTTTTC 421
OY 656 cagacaaaagaccgttgtgttctgtgataatgataatgataatgagagagagctgttctc 715
DB 422 CAGACCCAGACCGCCTGTGCTTGTTCATGAGATGAGGCCAACGGGGCGAGGTCTTC 481
OY 716 cattgtcgaagagcgggtgtctctgagagaccgcacacgttctatgtgcagaatt 775
DB 482 CACCTGTCCCGGGAAGGTGTGTTCTCGAGGACCGGGCCGCTTCTATGTGGCGTGAAT 541
OY 776 gtctgccttgagactatctacatctcggaaaga---tggtacggtatcatcaagt 832
DB 542 GTGTACGCCCTGTGACTACTGCACTGGAGAAAGACGTGTGACGGGACCTCAAGCTG 601
OY 833 gagaacttaagtctgcgaagaatgagccacataaataatatacagatttgcattgcaaa 892
DB 602 GAGAACCTCATGCTGAGCAAGGAGCGGNNCATTAAGATCAAGACTTGGCGGTGTCAAG 661
OY 893 gaagagatcacagatgcagccacatgaagacattctgtgcacatccagaatatctgcga 952
DB 662 GAGGGGATCAAGAGCGTCCACCAAGAGACCTTTTGGGCAACACTTAGTACCTGAGGCC 721
OY 953 ccagaggtgttagaagaataatgactatgcccagagagtagactgtgtgggccaagaggt 1012
DB 722 CCCGAGGTGCTGGAGAGACATGACTAGCGCGGAGTGTGAGTGTGTGGGGCTGGGGCTG 781
OY 1013 gtcatgtlaagaatgagtgtgtggaagttactcttctacacacagacatagaaact 1072
DB 782 GTCATGTACGAGATGATGTGCGGCTGCTTCTTACAAAGAGACCATGAGAGCTT 841
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QY 1073 ttgtaataataataatgaaga 1095  
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Db 842 TTTGAGCTCATCTCATGAGGA 864

RESULT 7  
BG668674 948 bp mRNA EST 01-MAY-2001  
LOCUS 602650859F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4763151 5',  
DEFINITION mRNA sequence.  
ACCESSION BG668674  
VERSION BG668674.1 GI:13918271  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 948)  
AUTHORS NIH-MGC <http://mgi.mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1C6M1618 row: f column: 16  
High quality sequence stop: 932.

FEATURES  
source  
1..948  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4763151"  
/clone\_1lb="NIH\_MGC\_48"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOT7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

BASE COUNT 217 a 274 c 292 g 165 t  
ORIGIN

Query Match 28.3%; Score 437.8; DB 11; Length 948;  
Best Local Similarity 70.1%; Pred. No. 9, 7e-97;  
Matches 660; Conservative 0; Mismatches 272; Indels 9; Gaps 5;

QY 5 gtcacatagagatgtccatttgaaagaagtgtggttcagaagaaggagagatat 64  
|||||  
Db 2 GGCACCATGAGCGACGTGCTATGTGAAGAGAGGTTGGCTGCACAAAGAGGAGGTAC 61

QY 65 ataaaaaactggagccagatagctctcttgaagaagatgagctcatcatagatat 124  
|||||  
Db 62 ATCAAGACCTGGCGGCGCACGCTACTTCTCTCAAGATGATGGCACCTTCATTTGCTAC 121

QY 125 aaagaanaactcaagatgtgattactta---tccctcaacaactttcagtgcga 181  
|||||  
Db 122 AAGGACGGCGCGAGATGTGGACCAAGTGAAGGCTCCCTCAACAACACTTCTGTGGGG 181

QY 182 aaatgcagttatgaagaagaagcaagaagcaacaacttaataatcagatgtc 241  
|||||  
Db 182 CAGTGCCACCTGATGAAGAGGAGCGCGCCCGCCACACACCTTCATCCGCTGCTG 241

QY 242 cagttgactactgttataagaagaacattcattagatatactccagaagaagaagaa 301  
|||||  
Db 242 CAGTGGACCACTGCTCATTCAGAACGACACCTTCCATGTGAGACTCTCTGAGAGGAGGAG 301

QY 302 tggacagaagactlccaggctgttagacagacagtcgcaagagcaagaagaagaatg 361  
|||||  
Db 302 TGGACAACCCGCCATCCAGACTGTGGCTGAGCGGCTCAAGAACGAGAGGAGGAGATG 361

QY 362 aattgtagtcacacttcacaaattgataatataatagaagaagaatgtagctctaca 421  
|||||  
Db 362 GACTTCGGTTCGGCTCACCACTGACAACTCAGGGGCTGAAGAGATGGAGGTGCTCCTG 421

QY 422 accatc---ataaagaagaagaatgatttgaatttgaatttgaatttgaatttga 478  
|||||  
Db 422 GCCAAGCCCAAGACCGCGGACCATTAAGCAAGATTTGAGTGAAGTGGTGGGCAAG 481

QY 479 ggcacttttggagaagttatttgttcgagaagaagcaagtgaaaaactatgtatg 538  
|||||  
Db 482 GGCACCTTTCGGCAAGGTGATCTGTGAAGGAGAACGCCACAGCGCGCTACTACGCCATG 541

QY 539 aagattctgaagaagaagatcatatttgaagaagaagtgagacacactcgaatga 598  
|||||  
Db 542 AAGATCCTCAAGAGAGATCATCTGCGCAAGACGAGGTGGC-CACACACTCACCGAG 600

QY 599 agcagagatlaaagaacactagacatcccttlaacatccttgaatattcctccag 658  
|||||  
Db 601 AACCGGCTCCTGAGAACTCAGACACCCCTTCTCAGACCCCTGAAGTACTTTTCCAG 660

QY 659 acaaaagaccgtttgtttgttgaatagttaatgtgagggcgagctgtttccat 718  
|||||  
Db 661 ACCCAGACCGGCTCTGTCTTCATGAGTACGCCAACAGGGGCGCAGCTGTCTTCCAC 720

QY 719 ttgtcgaagaagcgggtgttctcttgagagccgacacglttcatgtgcagaatt-gt 777  
|||||  
Db 721 CTGTCCCGGAGCGGTGTGTTCTCCGAGAGCGGCGCGCTTATGTGCGCTGAGATTGGT 780

QY 778 ctgtccttggaaatcct-acattccgaaagaattgttgaacgttgaatcgaattggaa 836  
|||||  
Db 781 GTACGCGCTGACTACTCTGACTGAGAGAGAGCTGCTGACCGGACCTCAAGCTGAGAG 840

QY 837 atctaagtctgcaaaagatgagccacataaaatcagaatttgaacttgcagaaga 896  
|||||  
Db 841 ACCTCATGCTGACGACGAGCGGCGACATTAAGATCAACACTTCGGGCTGTCCAGAGAG 900

QY 897 ggtacagatgagccaccatgaagaacatctgttgacct 937  
|||||  
Db 901 GGATCCAGGCGCGGTGCCACCATGAACCTTTGGGGCACACT 941

RESULT 8  
AL600183  
LOCUS AL600183 444 bp mRNA EST 14-AUG-2001  
DEFINITION DKFZP313J0132\_r1 313 (synonym: h1cc2) Homo sapiens cDNA clone  
DKFZP313J0132 5', mRNA sequence.  
ACCESSION AL600183  
VERSION AL600183.1 GI:15163689  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 444)  
AUTHORS Bloecker, H., Boecker, M., Brandt, P., Mewes, W., Well, B. and Wiemann  
S.  
TITLE (Bloecker, H., Boecker, M., Brandt, P., Mewes, W., Well, B. and Wiemann  
S.)  
JOURNAL Unpublished (1999)  
COMMENT MIPs  
Am Klopfersplitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ): Email: s.wiemannedtfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.

No s1 sequence available.  
This clone (DKFZ3J0132) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

Location/Qualifiers

## Source

1. 444  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZ3J0132"  
/clone\_id="313 (synonym: h1cc2)"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pTRIPlex2; Site\_1: SfilA; Site\_2: SfilB;  
cDNA-collection"

BASE COUNT 156 a 67 c 111 g 110 t

## ORIGIN

Query Match 26.8%; Score 415; DB 10; Length 444;  
Best Local Similarity 98.8%; Pred. No. 3.3e-91;  
Matches 418; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 234 ggggaagatgagcaagaactatccaggtgtatgacagacagactgcagaggaagaagg 353  
|||||  
Db 1 GGGGAAGATGACAGACAGCTATCCAGCGTGTAGCAGACAGACTGCAGAGCAAGAGAGC 60  
|||||  
OY 354 aagagatgaattgtatgccaacttaccacaattgataatagagagagagagatgagc 413  
|||||  
Db 61 AGAGATGATGATGTAGTCACTTCACTCAATGATATATATAGAGAGAGAGAGATGATG 120  
|||||  
OY 414 cctctacacaccatataaagaagacaatgaatgatttgactattgaaactactag 473  
|||||  
Db 121 CCTTCAACACCATCATATAAAGACAAATGATGATTTGACATATTGAAACTACTAG 180  
|||||  
OY 474 gtaagggcactttgggaagtatttgggttcgagagagagcaagtggaaataactatg 533  
|||||  
Db 181 GTAAAGGCACCTTTGGGAAAGTATTTGGTTCGAGAGAGCAAGTGAGAAATACTATG 240  
|||||  
OY 534 ctatgaagattctgaagaagaagatcatattgcaagaagatgaatgagacactctaa 593  
|||||  
Db 241 CTATGAAGATTGTGAAGAAAGATCATTTATTCAGAAAGATATAGTGCACACTCTTA 300  
|||||  
OY 594 ctgaaagcagagatlaaagaacactagacatcccttttaacatccttgaataatcct 653  
|||||  
Db 301 CTGAAGAGCAGATATTAAGAAGACACTAGACATCCCTTTTAACATCCTTGAATATCT 360  
|||||  
OY 654 tccagacaaagaaccggtttgttttggatggaataatgttaatggggcgagctgtttt 713  
|||||  
Db 361 TCCAGACAAAGACCGTGTGTTGTTGTCATGGAATATGTATATGGGGCGAGATGCACT 420  
|||||  
OY 714 tcc 716  
|||  
Db 421 TTC 423

## RESULT 9

## Bg748551

LOCUS Bg748551 843 bp mRNA EST 15-MAY-2001  
DEFINITION 60270624.F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4843042 5',  
mRNA sequence.

## ACCESSION

## Bg748551

## VERSION

## Bg748551.1

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 843)  
NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNI at:  
<http://image.llnl.gov>  
Plate: LLCMI678 row: 9 column: 11  
High quality sequence stop: 836.

## FEATURES

Location/Qualifiers

## Source

1. 843  
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/db\_xref="taxon:9606"  
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/clone\_id="NIH\_MGC\_43"  
/tissue\_type="normal pigmented retinal epithelium"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

BASE COUNT 186 a 238 c 265 g 154 t

## ORIGIN

Query Match 26.6%; Score 411; DB 11; Length 843;  
Best Local Similarity 71.2%; Pred. No. 3.5e-90;  
Matches 600; Conservative 0; Mismatches 235; Indels 8; Gaps 4;

OY 329 gacagacgcaagagcaagaagaagagagaatgaattgaagcacaattcacaaattgat 388  
|||||  
Db 1 GACGGCCTTCAAGAGAGGAGAGGAGGAGGAGGAGTTCGGTCCGGCTCCACCCAGTGC 60  
|||||  
OY 389 aatatagagagagagatgagtgatgcctctacacaccatcataaa---gaagacaatg 445  
|||||  
Db 61 AACTCAGGGGCTGAGAGAGATGAGAGTGTCCTCGGCCAACCCAGACCGCTGACATG 120  
|||||  
OY 446 aatgaatttgactattgaaactatgaatgaatgaatgaatgaatgaatgaatgaatga 505  
|||||  
Db 121 AACGAGTTTGAAGTACTGAAAGCTGCGGCAAGGCACTTTGCGCAAGTGATTCGTGTG 180  
|||||  
OY 506 cgaagagagcgaagtggaaataactatgctatgaagatctgaagaagaagaatcattat 565  
|||||  
Db 181 AAGGAGAAAGCCACAGCGCGTACTAGCGCAAGAAAGATCTCAAGAGAAAGATCTCGTG 240  
|||||  
OY 566 gcaagagatgaagtggcacacactctaaactgaagaagagatlaaagaacactagact 625  
|||||  
Db 241 GCCAAGAGCAGAGTGGCCACACACTCACCGAGAACCGGCTCTGACAGAACTCCAGGCAC 300  
|||||  
OY 626 cccttttaacatcccttgaataatccctctcagacaaagaacggtttgtttgttgatg 685  
|||||  
Db 301 CCTTCTCTCACAGCCCTGAAAGTACTTTCCAGACCCAGACCGGCTGCTTGTTCATG 360  
|||||  
OY 686 gaatatgttaatggggcgagctgttttccatcttgctgagagagcggggtgtctcagag 745  
|||||  
Db 361 GAGTACGCCAAGCGGGGCGAGCTGTTCTTCCACCTGCTCCGGGACGTTGTTCTCCAG 420  
|||||  
OY 746 gacgcacacggtttctatggtgcagaataatgtctgtccttgagactcttaattccgga 805  
|||||  
Db 421 GACCGGGCCGCTTCTATGGCGCTGAGATGTGTAGCCCTGAGTACTCTGACATCGGAG 480  
|||||  
OY 806 aaga---ttgttaccgtatctcaagttgaggaatcaatctcagacaaagaatgcac 862  
|||||  
Db 481 AAGAAAGTGTGTACTACGGGAGCTCAAGCTGGAGAACTCATCTGACACAGACGGGAC 540  
|||||



| QY         | 863  | ataaaattacagatttttggaatttgcacaaagaaggatcacagatgcagacccattgag    | 922                      |
|------------|--|---|--------------------------|
| Db         | 541  | ATTAAATCACACAGACTTGGGCTGTGCAGAGAGGGGATCTAGACGCTGCCACATGAAG      | 600                      |
| OY         | 923  | acattctgltgacactccagaatattcgtgacacagagagtgttagaagataatgactatgac | 982                      |
| Db         | 601  | ACCTTTTTCGGCGCACACCTGAGTACTGGCCCCCGAGGTGCTGAGACATGACTACGAC      | 660                      |
| OY         | 983  | cgagcagaagactgtaggggacctagggtttgtcatgatatgaaatattgtg-tggaggtt   | 1041                     |
| Db         | 661  | CTGTGAGTGTGAGTGTGTGGGGGCTGGGCGCTGTGCATGTACGAGATGATGTGCCGTGCT    | 720                      |
| OY         | 1042   | acccttctacacacacagccatgtagaaaacttttgaatataataatgaagaacattaa     | 1101                     |
| Db         | 721  | GCCCTTTCACAGACGAGACATGAGACACTTTTTCAGTTCATCCTCATGAGAGACA-TCG     | 779                      |
| OY         | 1102   | attctctgacacacctcttctagaatgcacaaatcatctgtcttcaggctcttgataaaga   | 1161                     |
| Db         | 780  | GTTCCTCCGGCAACGCTTGTCTCGAGGCCAAGTCTTGTTCACAGGGCTGCTCAGAAAGG     | 839                      |
| OY         | 1162   | tcg 1164  |                          |
| Db         | 840  | acc 842   |                          |
| RESULT     | 10   |   |                          |
| LOCUS      | BG913158   |   |                          |
| DEFINITION | BG913158   | 749 bp mRNA   | EST                      |
| ACCESSION  | 602811788  | NCI-CGAP_Brn67 Homo sapiens                                     | CDNA clone IMAGE:4943877 |
| VERSION    | 5', mRNA sequence.   |   |                          |
| KEYWORDS   | BG913158   | GI:14293634   |                          |
| SOURCE     | EST.   |   |                          |
| ORGANISM   | human.   |   |                          |
| REFERENCE  | Homo sapiens   |   |                          |
| AUTHORS    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi |   |                          |
| TITLE      | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.      |   |                          |
| JOURNAL    | NIH-MGC http://mgc.nci.nih.gov/                                  |   |                          |
| COMMENT    | National Institutes of Health, Mammalian Gene Collection (MGC)   |   |                          |
|            | Unpublished (1999)   |   |                          |
|            | Contact: Robert Strausberg, Ph.D.                                |   |                          |
|            | Email: cgapbs-remail.nih.gov                                     |   |                          |
|            | Tissue Procurement: David N. Louis, M.D.                         |   |                          |
|            | CNA Library Preparation: Life Technologies, Inc.                 |   |                          |
|            | CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)          |   |                          |
|            | DNA Sequencing by: Incyte Genomics, Inc.                         |   |                          |
|            | Clone distribution: MGC clone distribution information can be    |   |                          |
|            | found through the I.M.A.G.E. Consortium/LNL at:                  |   |                          |
|            | http://image.llnl.gov  |   |                          |
|            | Plate: LRAM10887 row: P column: 22                               |   |                          |
|            | High quality sequence stop: 747.                                 |   |                          |
| FEATURES   | Location/Qualifiers  |   |                          |
| source     | 1..749   |   |                          |
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|            | /db_xref="taxon:9606"  |   |                          |
|            | /clone_image="4943877"   |   |                          |
|            | /clone_id="NCI-CGAP_Brn67"                                       |   |                          |
|            | /tissue_type="anaplastic oligodendroglioma with 1p/19q           |   |                          |
|            | loss"  |   |                          |
|            | /lab_host="DH10B (TI phage-resistant)"                           |   |                          |
|            | /note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;          |   |                          |
|            | Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT          |   |                          |
|            | Average insert size 2.3 kb. Constructed by Life                  |   |                          |
|            | Technologies. Note: this is a NCI-CGAP Library."                 |   |                          |
| BASE COUNT | 159 a  | 219 c   | 228 g                    |
| ORIGIN     |  |   | 143 t                    |

|                           |        |                    |           |             |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match               | 26.48; | Score 408.2;       | DB 11;    | Length 749; |
| Best Local Similarity     | 72.5%; | Pred. No. 1.7e-89; |           |             |
| Matches 543; Conservative | 0;     | Mismatches 203;    | Indels 3; | Gaps 1;     |

[illegible]

|            |  |
|------------|--|
| RESULT     | 11   |
| LOCUS      | AA479072/c   |
| DEFINITION | AA479072 403 bp mRNA EST 08-AUG-1997   |
| CESSTION   | ZV171807.S1 Soares_hnMMPu_S1 Homo sapiens cDNA clone IMAGE:753876 3 similar to gb:U63167 RAC-ALPHA SERINE/THREONINE KINASE (HUMAN);.   |
| ERSION     | mRNA sequence.   |
| EYWORDS    | AA479072<br>AA479072.1 GI:2207628<br>EST.  |
| SOURCE     | human.<br>Homo sapiens   |
| ORGANISM   | Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Eumalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  |
| REFERENCE  | 1 (bases 1 to 403)   |
| AUTHORS    | Hillier,L., Allen,M., Bowles,L., Dubouque,T., Getsef,G., Jost,S.,<br>Kucaba,V., Lacy,M., Le,N., Lennon,G., Marra,M., Matlin,J., Moore,B,<br>Schellenberg,K., Steptoe,W., Tan,F., Theising,B., White,Y., Wylie,<br>T., Waterston,R. and Wilson,R. |
| TITLE      | WashU-Merck Est Project 1997   |
| JOURNAL    | Unpublished (1997)   |



## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -41m3 fwd. ET from Amersham  
High quality sequence stop: 370.

## FEATURES

## source

1. 403  
/organism="Homo sapiens"  
/db\_xref="GDB:5975747"  
/db\_xref="taxon:9606"  
/clone="IMAGE:753876"  
/clone\_1ib="Soares-NHMPu\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2bHM, pregnant uterus  
NBHPu, and fetal heart NBH19w) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT 87 a 94 c 69 g 153 t  
ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 403; DB 10; Length 403;  
Pred. No. 2.8e-88;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 29 gtgaaagaagttggttcagaagaaggagaaatataataaaacttgaagccaaatagac 88
DB 403 GTGAAAGAAGTTGGTTCAGAAAGGAGAGATATATATAAAACTGAGGCCAAGATATAC 344
OY 89 ttccctttgaagaagatggtcattcagaatataaagaagaactcaagatggtgat 148
DB 343 TTCCTTTGAAAGAGATGGCTCATATAGATATATAAGAAACCTCAAGATGGAT 284
OY 149 ttacctatccctcaaacactttcagtggaagaatgacagtttaagaagaagaaga 208
DB 283 TTACTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAGTTATGAAACAGAACGA 224
OY 209 ccaagccaaacacatttaacagatgttcacagtggaagactactgtlataagaagaaca 268
DB 223 CCAAGCCAAACACATTATATATCATGATGTCTCCAGTGCATCTTATAGAGAACAA 164
OY 269 ttccatgtatgatactccagaagaaggagaaatggaagactatccaggtctaga 328
DB 163 TTTTCATGTATGATCTCCAGAGAAAGGAAAGATGACAGAAAGCTATCCAGGCTGTAGCA 104
OY 329 gacacactgcaagcaagaagaagagaaatgaattgagttgacacactcacaaattgat 388
DB 103 GACAGACTGCAGAGCCAAAGAACAGAGAAATGAATTTGATGTCCAACTTCACAAATTGAT 44
OY 389 aatataagaagaagaagatgagatgctcttacaaccatcata 431
DB 43 AATATAAGAGAGAGATGATGCTCTACAAACCATCATCA 1

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## RESULT 12

LOCUS BG775183 1127 bp mRNA EST 15-MAY-2001  
DEFINITION 602650376F1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:4761259 5',  
mRNA sequence.

ACCESSION BG775183  
VERSION BG775183.1 GI:14045500  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1127)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTP/DRP

## COMMENT

cDNA library preparation: Ling Hong/Rubin Laboratory  
cDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LNCMI613 row: g column: 20  
High quality sequence stop: 770.

## FEATURES

## source

1. 1127  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4761259"  
/clone\_1ib="NIH\_MGC\_40"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: prostate; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming,  
directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GCCACAG(c). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using Zap-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT 253 a 336 c 330 g 208 t  
ORIGIN

## Query Match

Best Local Similarity 71.2%; Score 395.6; DB 11; Length 1127;  
Pred. No. 2.2e-86;  
Matches 594; Conservative 0; Mismatches 229; Indels 11; Gaps 5;

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OY 527 tactatgcatgaagaattctgaagaagaagatcattatgtcaagaagatgaatgagacac 586
DB 7 TACTAGCCATGAAGATCTCTCAAGAAGAGATCATGTCGCCAAGACAGAGTGGCCAC 66
OY 587 actctaactgaagcagaaglatuaagaacactagaacatcccttlttaacatccttga 646
DB 67 ACACCTACCGAGAACCGCTCTCGACAGACTCCAGCACCCCTTCTCACAGCCCTGAAG 126
OY 647 tattcttccaagaagaacacggttctgttttctgtatggaatataatgagggcgag 706
DB 127 TACTCTTTCACAGCCACGACCGCTCTCTTTGTATGATGAGTACCAACGGGGCGAG 186
OY 707 ctgttttccattgtcggagagagcggttctctcgaagacgcacacgttttcatagt 766
DB 187 CAGTTTTCACACTGTCCCGGAGAGCGTGTCTTCGAGAGACCGGCGCGCTTATGGC 246
OY 767 gagaagaattgtcttgccttgaactatcacatccgaaga--tctgtacgtgat 823
DB 247 GCTGAGATGTGTGACAGCCCTCGACTACCTCGAGAACAGAACTGATGTAACGGGAC 306
OY 824 ctcaagttggagaatctaagtctggaagaagaatgagcacaataaataacagatttga 883
DB 307 CTCGAAGCTGGAGAACTCATGTGTGACAGAGACGGGACACATTAAATCAACACTTGG 366
OY 884 ctctggaagaagagatcacagatgagacacatlaaagaacatctgtgtgaactccaaga 943
DB 367 CTGTGCAAGAGAGGATCAAGAGAGGTGCACCATTAAGACCTTTTGGCGCACACTTGA 426

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| BASE COUNT   | 223 a  | 275 c  | 305 g | 149 t |             |
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| ORIGIN   |  |        |       |       |             |
| Query Match  | 25.28; Score 390.2; DB 11; Length 952;                               |        |       |       |             |
| Best Local Similarity  | 71.68; Pred. No. 4.5e-85;  |        |       |       |             |
| Matches 569; Conservative 0; Mismatches 218; Indels 8; Gaps 4; |  |        |       |       |             |
| OY   | ctgtatagagaagaacatttcattgtatagatactccagagaaaggaagaaatgagacaagaag     | 311    |       |       |             |
| Db   | 2 CTGTGATCGAAGCGCACCTTCATGTGGAGACTCCGTGAGAGACGGGAGAGTGGACAAACCG      | 61     |       |       |             |
| OY   | 312 ctaccagagctgttgaacagacgactgcgcgagagcaagaagaagagagagatgaattgtagtc | 371    |       |       |             |
| Db   | 62 CCATCCAACACTGTGGCTGACGCGCTCAAGAAAGCAGAGAGAGAGAGATGACATCTCCGCT     | 121    |       |       |             |
| OY   | 372 caactcccaaatlalatataatagagagagagaagatgtaactgactctcaaccatc---     | 428    |       |       |             |
| Db   | 122 CGGGCTCACCCAGTGTACAACTCAGGGGCTGAAGAGATGAGATGCTCCCTGGCCAAAGCCCA   | 181    |       |       |             |
| OY   | 429 ataaagaagaacaaatgaaatgatttgactatttgaacctcagtgaaagacatttg         | 488    |       |       |             |
| Db   | 182 AGCACCGCGTGCACCTGTAACAGATTTGATCTGAACTCTGGGCAAGGGCACTTTCG         | 241    |       |       |             |
| OY   | 489 ggaagatatttggcttgtagagaaaggaagtgtgaaataactatagctatgaaagtttcga    | 548    |       |       |             |
| Db   | 242 GCMAAGTATCTGTGTGAAGGAGAAAGGCGCACAGGCGCTACTATACGCCATGAAAGATCTTCA  | 301    |       |       |             |
| OY   | 549 agaaagaagcatlataltcaagaagaatgaagtggcacacacttaactgaagaacagagat    | 608    |       |       |             |
| Db   | 302 AGAAGAGATCATCTGTGGCCAAAGACAGATGTGGCCCAACACTCAGCAGAAACGGCGTCC     | 361    |       |       |             |
| OY   | 609 taagaacacactagacatcccttlttaacatcccttgaatattccttccagacaaagaac     | 668    |       |       |             |
| Db   | 362 TGCAGAACTCCAGGACACCCCTTCCACAGCCCTGAAATCTTTCCAGACCCACAGCAC        | 421    |       |       |             |
| OY   | 669 gtttgtgtttgttgaatgaatgttaattgaagg--gcagagctgttttccatttctgaga     | 727    |       |       |             |
| Db   | 422 GCTCTGCTTGTGTCAATGAGATGACGCCAAAGGGGTGCGAGCTGTCTTCCACCTGTCCGG     | 481    |       |       |             |
| OY   | 728 gagcgagtgctctctcgtagagacgcacacgcttctcattgtagtcagaaatgtctcgtcttg  | 787    |       |       |             |
| Db   | 482 GAGCGTGTGTCTCCGAGAGACCGGGCCGCTTCTATGGCGGTGAATGTGTCAAGCCCTG       | 541    |       |       |             |
| OY   | 788 gaactatctacattccggaaga---ttgtgtacogtgaatctcaagtgtggaatcctaag     | 844    |       |       |             |
| Db   | 542 GACTACTCTGCACCTCGGAAGAACACTGTGTGTACCGCGGACCTCAAGCTGGAACACTCATG   | 601    |       |       |             |
| OY   | 845 ctgagcaaaagatgagcacaataaaatttcagaatttggactttgcaagaagagatcaca     | 904    |       |       |             |
| Db   | 602 CTGGCAAGAGACGGGCACTTAAATGATCAACAACCTTGGGCTGTGCAAGAGAGGGATTCAC    | 661    |       |       |             |
| OY   | 905 gatgagcacacacatlaagacattcgtgtgacactccagatatctcgcacagaggtgtca     | 964    |       |       |             |
| Db   | 662 GAGCGTGGCACCATTAATAAACCCTTTGGCGGCACACTGTAGTACTGTGGCCCGGAGGTGCTG  | 721    |       |       |             |
| OY   | 965 gaagaataatgactatgacgcgcagcagtagactgtgtggtgcttaagggtttgtcatgata   | 1024   |       |       |             |
| Db   | 722 GAGGACATATGACTACGGGCGTGAAGTGAAGTGAAGTGGG--CTGGGGGTGTGATGTAGACAC  | 780    |       |       |             |
| OY   | 1025 atgatgtgtgggaag 1039  |        |       |       |             |
| Db   | 781 CTGATGTGACAGGACG 795   |        |       |       |             |
| RESULT 14  |  |        |       |       |             |
| LOCUS  | BC747687   | 786 bp | mRNA  | EST   | 15-MAY-2001 |
| DEFINITION   | 60270515BP1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4841799 5',     |        |       |       |             |
| ACCESSION  | BC747687   |        |       |       |             |
| VERSION  | BC747687.1   |        |       |       |             |
| KEYWORDS   | EST, GI:14058340   |        |       |       |             |

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 786)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L16M1675 row: c column: 16  
High quality sequence stop: 760.  
Location/Qualifiers

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/note="Organ: eye; Vector: pOTB1; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(S). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 177 a 219 c 253 g 137 t  
ORIGIN

Query Match 24.9%; Score 385; DB 11; Length 786;  
Best Local Similarity 71.6%; Pred. No. 8.1e-84;  
Matches 562; Conservative 0; Mismatches 215; Indels 8; Gaps 4;

QY 252 cgttatagagaagaattcattatgtagatattccagagagaagaagaattgagcgaag 311  
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QY 312 ctatccagcgttagcagacagacgagcgaagaagaagaagaagaattgtagtc 371  
DB 62 ccattccagactgtgctgacgagcgcctcacaacacagagagagagatggacttccggt 121  
QY 372 caacttcacaaatgataatagagagaagaagaatgtagcctctacacccatc--- 428  
DB 122 cggcgctacccagctgac 181  
QY 429 ataaaaagaagaagaatgtagtattgtagtattgtagtattgtagtattgtagtattg 488  
DB 182 accaccgctgac 241  
QY 489 ggaagaattattgttgcgagaagaagaagaagaagaagaagaagaagaagaagaaga 548  
DB 242 gcaagtgatctctggaagagagagagagagagagagagagagagagagagagag 301  
QY 549 aagaagaagcattattgcaagaagagagagagagagagagagagagagagagagagat 608  
DB 302 aagaagaagcattattgcaagaagagagagagagagagagagagagagagagagagat 361  
QY 609 taagaagacactagacatcccttttaacatccttccctccagacagaagagac 668  
DB 362 tgcagaaatgcagagcacccttctcagacagccttctcagacagcaccacacacac 421  
QY 669 gtttggttttgtagatgatatgttaaggggagagctgtttccatttgtagag 728

DB 422 gcctctgcttctgcatgagatgacccacagggggcagagctgttctccactgtcccg 481  
QY 729 aggggtgttctcttgagagccgacacgcttctatgttgagaaattgtctgtccttg 788  
DB 482 agcgtgtgttctccagagacccggcctctctatgagcctgagatgttgcacgctcg 541  
QY 789 actatcatcttcggaaga---ttgtgacgtgtagctcaagttggaagatcatgac 845  
DB 542 actactgcactctggagagacagctgtgacggagacactcaacctggagaaacctatgc 601  
QY 846 tggacaagaatggtccacataaaatacagaatttggacttgcagaagaagatcacag 905  
DB 602 tggacaagaagcggcagacattatgagatcagacacttgcggctgtgcagagagagac 661  
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QY 966 aaga-taatgacatggtccgagagatgagctgt-ggggcctaggggttgcattatga 1023  
DB 722 agacccaatgactacggcgtgcatgtagctgtgggggctggcgtgcatgtagca 781  
QY 1024 aatga 1028  
DB 782 gatga 786

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AA530983/c n110h03.s1 NCI-CGAP Pr22 Homo sapiens CDNA clone IMAGE:985973 3'  
LOCUS similar to gb:M63167 RAC-ALPHA SERINE/THREONINE KINASE (HUMAN);,  
DEFINITION mRNA sequence.  
ACCESSION AA530983 GI:2273689  
VERSION AA530983  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 387)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov).  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/biopr/image/image.html](http://www.bio.llnl.gov/biopr/image/image.html)  
Seq primer: 40m13 fwd. RT from Amersham  
High quality sequence stop: 385.  
Location/Qualifiers

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/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pRT30-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized, and was

